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1017

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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/965,631

DATE: 10/18/2001

TIME: 09:53:30

Input Set : A:\LEX-0241-USA SEQLIST.txt

Output Set: N:\CRF3\10182001\I965631.raw

ENTERED

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4 <110> APPLICANT: Friddle, Carl Johan
5 Hilbun, Erin
7 <120> TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the Same
9 <130> FILE REFERENCE: LEX-0241-USA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/965,631
C--> 11 <141> CURRENT FILING DATE: 2001-09-27
11 <150> PRIOR APPLICATION NUMBER: US 60/236,689
12 <151> PRIOR FILING DATE: 2000-09-29
14 <160> NUMBER OF SEQ ID NOS: 7
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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19 <211> LENGTH: 966
20 <212> TYPE: DNA
21 <213> ORGANISM: homo sapiens
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25 ccagagcggg aggtagtcgt tcccatccga ctggaccggg acattaacgg ccgcgcgtac 120
26 tactggcggg gtcccaggga ctccggggat cagggactca tttttcagat cacagcattt 180
27 caggaggact ttacctaca cctgacgccg gatgctcagt tcttggctcc cccttctccc 240
28 actgagcatt tgggcgtccc cctccagggg ctccaccggg gctcttcaga cctgcgcacg 300
29 tgcctctatt ctggggaact gaacgcggag ccggactcgt tcgctgctgt gaggctgtgc 360
30 ggggggctcc gcggagcctt tggctaccga ggcgccagat atgtcattag cccgctgcce 420
31 aatgctagcg cgccggcgcc gcagcgcaac agccaggggc cacacottct ccagcgccgg 480
32 ggtgttccgg gcgggcccct cggagacccc acctctcgtc gcgggggtgc ctcgggctgg 540
33 aaccccgcca tctacggggc cctggacctt tacaagccgc ggcggggcgg cttcggggag 600
34 agtcgtagcc ggccgaggtc tggcgcgccc aagcgtttcg tctctatccc gcggtacgtg 660
35 gagacgctgg tggctcgcca cagatcaaat gtcaagtccc acggcgcgga cctggaacat 720
36 tatctgtcga cgctgctggc aacggcgccg cgactctacc gccatccag catctcaac 780
37 cccatcaaca tcgttgtgtt caaggtgctg cttcttagag atcgtgactc cgggcccaga 840
38 gtccaccgga atgcggccct cagcgtgcgc aactctgtg cctggcagaa gaagctgaac 900
39 aaagtgaagt acaagcaccg ccagttactgg gacactgcca tctctttcac caggcaggag 960
40 agttga
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 321
44 <212> TYPE: PRT
45 <213> ORGANISM: homo sapiens
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50 Gly Gly Ser Glu Pro Glu Arg Glu Val Val Pro Ile Arg Leu Asp
51 20 25 30
52 Pro Asp Ile Asn Gly Arg Arg Tyr Tyr Trp Arg Gly Pro Glu Asp Ser
53 35 40 45
54 Gly Asp Gln Gly Leu Ile Phe Gln Ile Thr Ala Phe Gln Glu Asp Phe
55 50 55 60
56 Tyr Leu His Leu Thr Pro Asp Ala Gln Phe Leu Ala Pro Ala Phe Ser
57 65 70 75 80

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58 Thr Glu His Leu Gly Val Pro Leu Gln Gly Leu Thr Gly Gly Ser Ser
59      85      90      95
60 Asp Leu Arg Arg Cys Phe Tyr Ser Gly Asp Val Asn Ala Glu Pro Asp
61      100      105      110
62 Ser Phe Ala Ala Val Ser Leu Cys Gly Gly Leu Arg Gly Ala Phe Gly
63      115      120      125
64 Tyr Arg Gly Ala Glu Tyr Val Ile Ser Pro Leu Pro Asn Ala Ser Ala
65      130      135      140
66 Pro Ala Ala Gln Arg Asn Ser Gln Gly Ala His Leu Leu Gln Arg Arg
67 145      150      155      160
68 Gly Val Pro Gly Gly Pro Ser Gly Asp Pro Thr Ser Arg Cys Gly Val
69      165      170      175
70 Ala Ser Gly Trp Asn Pro Ala Ile Leu Arg Ala Leu Asp Pro Tyr Lys
71      180      185      190
72 Pro Arg Arg Ala Gly Phe Gly Glu Ser Arg Ser Arg Arg Arg Ser Gly
73      195      200      205
74 Arg Ala Lys Arg Phe Val Ser Ile Pro Arg Tyr Val Glu Thr Leu Val
75      210      215      220
76 Val Ala Asp Glu Ser Met Val Lys Phe His Gly Ala Asp Leu Glu His
77 225      230      235      240
78 Tyr Leu Leu Thr Leu Leu Ala Thr Ala Ala Arg Leu Tyr Arg His Pro
79      245      250      255
80 Ser Ile Leu Asn Pro Ile Asn Ile Val Val Val Lys Val Leu Leu Leu
81      260      265      270
82 Arg Asp Arg Asp Ser Gly Pro Lys Val Thr Gly Asn Ala Ala Leu Thr
83      275      280      285
84 Leu Arg Asn Phe Cys Ala Trp Gln Lys Lys Leu Asn Lys Val Ser Asp
85      290      295      300
86 Lys His Pro Glu Tyr Trp Asp Thr Ala Ile Leu Phe Thr Arg Gln Glu
87 305      310      315      320
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92 <211> LENGTH: 2853
93 <212> TYPE: DNA
94 <213> ORGANISM: homo sapiens
96 <400> SEQUENCE: 3
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98 ccagagcggg aggtagtctg tccatccga ctggaccgg acattaacgg ccgcgcctac 120
99 tactggcggg gtcccaggga ctccgggat cagggactca ttttcagat cacagcattt 180
100 caggaggact tttaoctaca cctgacgcgg gatgctcagt tcttggctcc cgcttctccc 240
101 actgagcacc tgggcgtccc cctccagggg ctcaccgggg gctcttcaga cctgcgacgc 300
102 tgtctctatt ctggggacgt gaaccgcgag ccggactcgt tcgctgctgt gaggctgtgc 360
103 ggggggctcc gcggagcctt tggtaccga gcgcgcgagt atgtcaatag cccgctgcc 420
104 aatgctagcg cgccggcgcc gcagcgcaac agccaggggc cacaccttct ccagcgccgg 480
105 ggtgttcocg gcgggccttc cggagacccc acctctcgt cgggggtggc ctccggctgg 540
106 aaccgcccca tctacgggc cctggacct tacaagccgc gggggcgagg ctccggggag 600
107 agtcgtagcc ggcgcaggtc tgggcgcgcc aagcgtttcg tctctatccc gcggtacgtg 660
108 gagacgctg tggtcgcgga cgatccaatg gtcaagttcc acggcgcgga cctggaacat 720
109 tatctgctga cgctgctggc aacggcgggc cgactctacc gccatcccat catctccaac 780

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110 cccatcaaca tctgttgtgt caaggtgctg cttcttagag atcgtgactc cgggcccacg 840
111 gtcaccggca atcgggccct gacgtctgcg aactctctgt cctggcagaa gaagctgaac 900
112 aaagtgtagt acaagcacc cagactctgg gacactgcca tcctcttcac caggcaggac 960
113 ctgtgtggag ccaccacctg tgacacctg ggcactggct atgtgggtac catgtgtgac 1020
114 cccaagagaa gctgctctgt cattggagac gatgggcttc catcagcctt caccactgcc 1080
115 cacgagctgg gccacgtgtt caacatgccc catgacaatg tgaaagtctg tgaggagggt 1140
116 tttgggaagc tccgagccaa ccacatgatg tcccgcacc tcattccagat cgaccgtgcc 1200
117 aacccctggt cagcctgcag tgetgccatc atcaccgact tctgggacag cgggcacggt 1260
118 gactgctctc tggaccaaacc cagcaagccc atctccctgc ccgaggatct gccggggccc 1320
119 agctacaccc tggaccagca gtgcgagctg gcttttggtg tgggctccaa gccctgtctc 1380
120 tacatgcagt actgcaccaaa gctgtgtgtc accgggaagg ccaagggcaa gatggtgtgc 1440
121 cacaccggcc acttccccct ggcgatggcg aacagctgtg gcgaggggcaa gctctgcctc 1500
122 aaaggggccc gctgtggagag acacaacctc acaagcaca ggggtgatgg ttctcggggc 1560
123 aaatgggagt cctatggccc ctgtcgcgcg acatgtgtgt ggggctgtca gctggccagg 1620
124 aggcagtga ccaaccacc cctgcacaac gggggcaagt actcgaggag agtgagggtg 1680
125 aaataccgat cctgcaatct ggagccctgc cccagctcag cctccggaaa gactctccgg 1740
126 gaggagcagt gtgaggcttt caacggctac aaccacagca ccaacggctt cactctcgcc 1800
127 gtggcctggg tgcccaagta ctccggctgt tctcccggg acaagtgcaa gctcatctgc 1860
128 cgagccaaat gcactggcta cttctatgtg ctggaccaca aggtggtgga cggcagctgt 1920
129 tgcctctctg actccacctc cgtctgtgtc caaggcaagt gcatacaggc tggctgtgat 1980
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132 gccatccccg caggcgctcc aagcatcgac atcccgagc gcggttacaa agggctgata 2160
133 ggggatgaca actactggc tctgaagaac agccaaggc agtacctgt caacgggcat 2220
134 tctgtgtgtg cggcggttga gcggggacct gtggtgaagg gcagtgctct gcggtacagc 2280
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136 gtggaggtcc tctccgtggg gaagatgaca ccgcccggg tccgtactc cttctatctg 2400
137 cccaagagcg ctggggagga caagtctctc catcccaagg accccggggg accctctgtc 2460
138 ttgcacaaac gcgtctcag cctctccaac caggtggagc agccggagca caggccccct 2520
139 gcacgctggg tggctggcag ctggggggcc tgcctcgca gctcgggcag tggcctgacg 2580
140 aagcggggcg tggactgtcg gggctccgcc gggcagcgca cggctccctc cgtgtatgca 2640
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142 cctgtgtcac cctgctccaa gagctcgggc cggggatttc agaggcgctc acctcaagt 2760
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147 <211> LENGTH: 950
148 <212> TYPE: PRT
149 <213> ORGANISM: homo sapiens
151 <400> SEQUENCE: 4
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155 20 25 30
156 Pro Asp Ile Asn Gly Arg Arg Tyr Tyr Trp Arg Gly Pro Glu Asp Ser
157 35 40 45
158 Gly Asp Gln Gly Leu Ile Phe Gln Ile Thr Ala Phe Gln Glu Asp Phe
159 50 55 60
160 Tyr Leu His Leu Thr Pro Asp Ala Gln Phe Leu Ala Pro Ala Phe Ser

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161 65              70              75              80
162 Thr Glu His Leu Gly Val Pro Leu Gln Gly Leu Thr Gly Gly Ser Ser
163                               85              90              95
164 Asp Leu Arg Arg Cys Phe Tyr Ser Gly Asp Val Asn Ala Glu Pro Asp
165                               100              105              110
166 Ser Phe Ala Ala Val Ser Leu Cys Gly Gly Leu Arg Gly Ala Phe Gly
167                               115              120              125
168 Tyr Arg Gly Ala Glu Tyr Val Ile Ser Pro Leu Pro Asn Ala Ser Ala
169                               130              135              140
170 Pro Ala Ala Gln Arg Asn Ser Gln Gly Ala His Leu Leu Gln Arg Arg
171                               145              150              155
172 Gly Val Pro Gly Gly Pro Ser Gly Asp Pro Thr Ser Arg Cys Gly Val
173                               165              170              175
174 Ala Ser Gly Trp Asn Pro Ala Ile Leu Arg Ala Leu Asp Pro Tyr Lys
175                               180              185              190
176 Pro Arg Arg Ala Gly Phe Gly Glu Ser Arg Ser Arg Arg Arg Ser Gly
177                               195              200              205
178 Arg Ala Lys Arg Phe Val Ser Ile Pro Arg Tyr Val Glu Thr Leu Val
179                               210              215              220
180 Val Ala Asp Glu Ser Met Val Lys Phe His Gly Ala Asp Leu Glu His
181                               225              230              235
182 Tyr Leu Leu Thr Leu Leu Ala Thr Ala Ala Arg Leu Tyr Arg His Pro
183                               245              250              255
184 Ser Ile Leu Asn Pro Ile Asn Ile Val Val Val Lys Val Leu Leu Leu
185                               260              265              270
186 Arg Asp Arg Asp Ser Gly Pro Lys Val Thr Gly Asn Ala Ala Leu Thr
187                               275              280              285
188 Leu Arg Asn Phe Cys Ala Trp Gln Lys Lys Leu Asn Lys Val Ser Asp
189                               290              295              300
190 Lys His Pro Glu Tyr Trp Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp
191                               305              310              315
192 Leu Cys Gly Ala Thr Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly
193                               325              330              335
194 Thr Met Cys Asp Pro Lys Arg Ser Cys Ser Val Ile Glu Asp Asp Gly
195                               340              345              350
196 Leu Pro Ser Ala Phe Thr Thr Ala His Glu Leu Gly His Val Phe Asn
197                               355              360              365
198 Met Pro His Asp Asn Val Lys Val Cys Glu Glu Val Phe Gly Lys Leu
199                               370              375              380
200 Arg Ala Asn His Met Met Ser Pro Thr Leu Ile Gln Ile Asp Arg Ala
201                               385              390              395
202 Asn Pro Trp Ser Ala Cys Ser Ala Ala Ile Ile Thr Asp Phe Leu Asp
203                               405              410              415
204 Ser Gly His Gly Asp Cys Leu Leu Asp Gln Pro Ser Lys Pro Ile Ser
205                               420              425              430
206 Leu Pro Glu Asp Leu Pro Gly Ala Ser Tyr Thr Leu Ser Gln Gln Cys
207                               435              440              445
208 Glu Leu Ala Phe Gly Val Gly Ser Lys Pro Cys Pro Tyr Met Gln Tyr
209                               450              455              460

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210 Cys Thr Lys Leu Trp Cys Thr Gly Lys Ala Lys Gly Gln Met Val Cys
211 465 470 475 480
212 Gln Thr Arg His Phe Pro Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly
213 485 490 495
214 Lys Leu Cys Leu Lys Gly Ala Cys Val Glu Arg His Asn Leu Asn Lys
215 500 505 510
216 His Arg Val Asp Gly Ser Trp Ala Lys Trp Asp Pro Tyr Gly Pro Cys
217 515 520 525
218 Ser Arg Thr Cys Gly Gly Gly Val Gln Leu Ala Arg Arg Gln Cys Thr
219 530 535 540
220 Asn Pro Thr Pro Ala Asn Gly Gly Lys Tyr Cys Glu Gly Val Arg Val
221 545 550 555 560
222 Lys Tyr Arg Ser Cys Asn Leu Glu Pro Cys Pro Ser Ser Ala Ser Gly
223 565 570 575
224 Lys Ser Phe Arg Glu Glu Gln Cys Glu Ala Phe Asn Gly Tyr Asn His
225 580 585 590
226 Ser Thr Asn Arg Leu Thr Leu Ala Val Ala Trp Val Pro Lys Tyr Ser
227 595 600 605
228 Gly Val Ser Pro Arg Asp Lys Cys Lys Leu Ile Cys Arg Ala Asn Gly
229 610 615 620
230 Thr Gly Tyr Phe Tyr Val Leu Ala Pro Lys Val Val Asp Gly Thr Leu
231 625 630 635 640
232 Cys Ser Pro Asp Ser Thr Ser Val Cys Val Gln Gly Lys Cys Ile Lys
233 645 650 655
234 Ala Gly Cys Asp Gly Asn Leu Gly Ser Lys Lys Arg Phe Asp Lys Cys
235 660 665 670
236 Gly Val Cys Gly Gly Asp Asn Lys Ser Cys Lys Lys Val Thr Gly Leu
237 675 680 685
238 Phe Thr Lys Pro Met His Gly Tyr Asn Phe Val Val Ala Ile Pro Ala
239 690 695 700
240 Gly Ala Ser Ser Ile Asp Ile Arg Gln Arg Gly Tyr Lys Gly Leu Ile
241 705 710 715 720
242 Gly Asp Asp Asn Tyr Leu Ala Leu Lys Asn Ser Gln Gly Lys Tyr Leu
243 725 730 735
244 Leu Asn Gly His Phe Val Val Ser Ala Val Glu Arg Asp Leu Val Val
245 740 745 750
246 Lys Gly Ser Leu Leu Arg Tyr Ser Gly Thr Gly Thr Ala Val Glu Ser
247 755 760 765
248 Leu Gln Ala Ser Arg Pro Ile Leu Glu Pro Leu Thr Val Glu Val Leu
249 770 775 780
250 Ser Val Gly Lys Met Thr Pro Pro Arg Val Arg Tyr Ser Phe Tyr Leu
251 785 790 795 800
252 Pro Lys Glu Pro Arg Glu Asp Lys Ser Ser His Pro Lys Asp Pro Arg
253 805 810 815
254 Gly Pro Ser Val Leu His Asn Ser Val Leu Ser Leu Ser Asn Gln Val
255 820 825 830
256 Glu Gln Pro Asp Asp Arg Pro Pro Ala Arg Trp Val Ala Gly Ser Trp
257 835 840 845
258 Gly Pro Cys Ser Ala Ser Cys Gly Ser Gly Leu Gln Lys Arg Ala Val

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VERIFICATION SUMMARY

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DATE: 10/18/2001

TIME: 09:53:31

Input Set : A:\LEX-0241-USA SEQLIST.txt

Output Set: N:\CRF3\10182001\I965631.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date